



06 MAY 2008

COMMISSIONER FOR PATENTS  
UNITED STATES PATENT AND TRADEMARK OFFICE  
P.O. Box 1450  
ALEXANDRIA, VA 22313-1450  
www.uspto.gov

WIGGIN AND DANA LLP  
ATTENTION: PATENT DOCKETING  
ONE CENTURY TOWER, P.O. BOX 1832  
NEW HAVEN CT 06508-1832

In re Application of	:	DECISION ON
HELLSTROM et al	:	
Application No. 10/581,761	:	
PCT No.: PCT/SE2004/001814	:	
Int. Filing Date: 06 December 2004	:	
Priority Date: 05 December 2003	:	PETITION UNDER
Attorney's Docket No.: 0208/76419-PCT-US	:	
For: METHOD OF USE...	:	
METHOD OF USE THEREOF	:	37 CFR 1.137 (b)

This decision is in response to applicant's "RESPONSE TO NOTIFICATION OF MISSING REQUIREMENTS FILED WITH A PETITION UNDER 37 CFR 1.137(b)," filed on 10 April 2008.

### **BACKGROUND**

On 06 December 2004, this international application was filed, which claimed priority to an application filed on 05 December 2003. The deadline for paying the basic national fee in the United States under 35 U.S.C. 371 and 37 CFR 1.495 was 05 June 2006.

On 05 June 2006, applicants filed a Transmittal letter for entry into the national stage in the United States Patent and Trademark Office (USPTO), which was accompanied by, the basic national fee. No executed declaration or oath was filed at such time.

On 13 February 2007, the United States Designated/Elected Office mailed a Notification of Missing Requirements under 35 U.S.C. 371 (Form PCT/DO/EO/905) indicating that the oath or declaration complying with 37 CFR 1.497(a) and (b), identifying the application by the International application number and International filing date and that a copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e)." The Notice stated that the above items must be furnished within the time period set forth. The notification set a two months time limit or 32 months from the priority date for the application, whichever is later to respond, and that failure to properly respond would result in abandonment.

On 08 February 2008, the United States Patent and Trademark Office mailed the Notification of Abandonment (PCT/DO/EO/909) because applicant has failed to respond to the notification of MISSING REQUIREMENTS (Form PCT/DO/EO/905), mailed 02/13/2007 within the time period set therein.

On 10 April 2008, applicants filed the instant petition under 37 CFR 1.137(b), which was accompanied by the petition fee, an executed declaration and a copy of the sequence listing in computer-readable form (CRF).

### DISCUSSION

A grantable petition to revive an abandoned application under 37 CFR 1.137(b) must be accompanied by (1) the required reply, unless previously filed. In a nonprovisional application abandoned for failure to prosecute, the required reply may be met by the filing of a continuing application; (2) the petition fee as set forth in § 1.17(m); and (3) a statement that the entire delay in filing the required reply from the due date for the reply until the filing of a grantable petition pursuant to this paragraph was unintentional. The Commissioner may require additional information where there is a question whether the delay was unintentional; and (4) any terminal disclaimer (and fee as set forth in § 1.20 (d)) required pursuant to paragraph (c) of this section.

Petitioner has provided: (1) the proper reply by submitting a properly executed declaration, but the copy of the sequence listing in computer-readable form is flawed (2) the petition fee set forth in § 1.17(m) and (3) the proper statement under 137(b)(3). In this application, no terminal disclaimer is required.

Accordingly, the petition is deemed to satisfy items (2) - (4) but not item (1) under 37 CFR 1.137(b). As such, the application remains abandoned.

### DECISION

The petition under 37 CFR 1.137(b) is **DISMISSED** without prejudice.

If reconsideration of the merits of the petition under 37 CFR 1.137(b) is desired, applicant must file a request for reconsideration within **TWO (2) MONTHS** from the mail date of this Decision. Failure to timely submit the proper reply will result in abandonment of the application. Any reconsideration request should include a cover letter entitled "Renewed Petition Under 37 CFR 1.137(b)." Extensions of time are available under 37 CFR 1.136(a).

Any further correspondence with respect to this matter should be addressed to the Mail Stop PCT, Commissioner for Patents, Office of PCT Legal Administration, P.O. Box 1450, Alexandria, Virginia 22313-1450, with the contents of the letter marked to the attention of the Office of PCT Legal Administration.



Rafael Bacares

PCT Legal Examiner

PCT Legal Office

Telephone: (571) 272-3276

Facsimile : (571) 273-0459

Enc: Error report on flawed CRF

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=4; day=30; hr=20; min=16; sec=49; ms=897; ]

=====

\*\*\*\*\*

Reviewer Comments:

SEQUENCE LISTING

<110> Hellström, Mats  
Wallgard, Elisabet  
Kalén, Mattias

Please remove the foreign accent marks in the first and third  
applicant's names; foreign accent marks are non-ACII characters, which  
cannot be processed.

<120> ANGIOGENESIS-AFFECTING POLYPEPTIDES, PROTEINS, AND COMPOSITIONS,  
AND METHODS OF USE THEREOF

The above <120> response exceeds the Sequence Rules' required 72-  
character line limit: please adjust the line, by inserting hard  
returns.

(from the end of Sequence 52)

Ser Cys Ser Leu Glu Pro Ser Ala Pro Glu Asp Leu Leu  
850 855 860

Please remove the "1" above, which appears at the end of the submitted  
file.

Application No: 10581761 Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-15 14:49:57.985  
Finished: 2008-04-15 14:50:00.843  
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 858 ms  
Total Warnings: 30  
Total Errors: 2  
No. of SeqIDs Defined: 52  
Actual SeqID Count: 52

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (23)
W 402	Undefined organism found in <213> in SEQ ID (24)
W 402	Undefined organism found in <213> in SEQ ID (25)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (34)

Input Set:

Output Set:

Started: 2008-04-15 14:49:57.985  
Finished: 2008-04-15 14:50:00.843  
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 858 ms  
Total Warnings: 30  
Total Errors: 2  
No. of SeqIDs Defined: 52  
Actual SeqID Count: 52

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (52)

<210> 1  
<211> 736  
<212> DNA  
<213> Murinae gen. sp.

<400> 1  
gtgatccagg atccgaagag gcccggagca ggagcatggc gtcgtcgggg tcggtgcagc 60  
agctgcccct ggtgctgctg atgttgctgt tggcgagtgc ggcacggggc agactctact 120  
tccgctcggg ccagacttgc taccatccca ttcgcgggga ccagctgget ctgctggggc 180  
gcaggactta tctcggccg catgagtacc tgtccccagc ggatctcccc aagaattggg 240  
actggagaaa tgtgaacggt gtcaactatg ccagcgtcac caggaaccag cacatcccac 300  
agtactgtgg ttctgctgg gccacggca gcaccagtgc catggcagac cgaatcaaca 360  
tcaagaggaa aggtgcatgg cctccatcc tgctgtccgt acagaatgtc attgactgtg 420  
gcaatgctgg ctcttgtaga gggggcaatg accttccggt gtgggagtat gccacaagc 480  
atggcatccc cgatgagacc tgcaacaact accaggcaag gaccaagact gtgacaagtt 540  
taaccagtgt gggacctgca ctgaattcaa agagtgtcac accatccaga attacaccct 600  
ctggagagtg ggtgattacg gtccctgtcc gggagggaga agatgatggc gagatctatg 660  
ccaatgggcc catcagctgc gggataatgg gcaccagaga tgatgtctaa ctacactggg 720  
ggcatctatg ctgagc 736

<210> 2  
<211> 1404  
<212> DNA  
<213> Murinae gen. sp.

<400> 2  
aaaggaccgg gcggggcgct ccgagcgctt gggcctgcgg gtcgggtcaa gaggtcgaag 60  
gtgctgcgct tgatccagga tccgaattgg cccggagcag gagcatggcg tcgtcggggt 120  
cggtgcagca gctgcccctg gtgctgctga tgttgctgtt ggcgagtgcg gcacggggca 180  
gactctactt ccgctcgggc cagacttgct accatcccat tcgcggggac cagctggctc 240  
tgctggggcg caggacttat cctcggccgc atgagtacct gtccccagcg gatctcccca 300  
agaattggga ctggagaaat gtgaacggtg tcaactatgc cagcgtcacc aggaaccagc 360  
acatcccaca gtactgtggt tctgctggg cccacggcag caccagtgc atggcagacc 420  
gaatcaacat caagaggaaa ggtgcatggc cctccatcct gctgtccgta cagaatgtca 480  
ttgactgtgg caatgctggc tcttgtaga ggggcaatga ccttccggtg tgggagtatg 540

cccacaagca tggcatcccc gatgagacct gcaacaacta ccaggccaag gaccaagact 600  
 gtgacaagtt taaccagtgt gggacctgca ctgaattcaa agagtgtcac accatccaga 660  
 attacaccct ctggagagtg ggtgattacg gctccctgtc cgggagggag aagatgatgg 720  
 ccgagatcta tgccaatggt cccatcagct gcgggataat ggcaacagag atgatgtcta 780  
 actacactgg gggcatctat gctgagcacc aggaccaggc cgttatcaac cacatcatct 840  
 ctgtagctgg ctggggtgtc agcaacgatg gcatcgagta ctggattgtc cgaaattcat 900  
 ggggcgaacc ctggggtgag aaaggctgga tgaggatcgt gaccagcacc tacaaggag 960  
 gcacaggtga cagctacaac cttgccatcg agagtgcctg cacatttggg gacccattg 1020  
 tttaggtaga tgtctctgga agcagcgtg tgaaccatga cagggagggg tgattaatta 1080  
 ctgacactgg acatgtccag acagctataa acagtgcttg tggacatgag gaccagagtg 1140  
 tggactgcat cccgagagga gacggtaaag gatgaaacac aactgcactg ggaccctccg 1200  
 ccgtaccctc caggcctgcc tcctccacca ctgagccctc caggcctgcc tcctcttcta 1260  
 cagtgccttg cttcagccac ccggagaaga gagctatggt ttaggacagc tcaacttata 1320  
 accagatctg gagccctgga atccatggga ggggggaaca agtccagact gcttaagaaa 1380  
 tgagtaaaat atctggcttc ccac 1404

<210> 3  
 <211> 306  
 <212> PRT  
 <213> Murinae gen. sp.

<400> 3

Met Ala Ser Ser Gly Ser Val Gln Gln Leu Pro Leu Val Leu Leu Met  
 1 5 10 15

Leu Leu Leu Ala Ser Ala Ala Arg Ala Arg Leu Tyr Phe Arg Ser Gly  
 20 25 30

Gln Thr Cys Tyr His Pro Ile Arg Gly Asp Gln Leu Ala Leu Leu Gly  
 35 40 45

Arg Arg Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu  
 50 55 60

Pro Lys Asn Trp Asp Trp Arg Asn Val Asn Gly Val Asn Tyr Ala Ser  
 65 70 75 80

Val	Thr	Arg	Asn	Gln	His	Ile	Pro	Gln	Tyr	Cys	Gly	Ser	Cys	Trp	Ala	85	90	95	
His	Gly	Ser	Thr	Ser	Ala	Met	Ala	Asp	Arg	Ile	Asn	Ile	Lys	Arg	Lys	100	105	110	
Gly	Ala	Trp	Pro	Ser	Ile	Leu	Leu	Ser	Val	Gln	Asn	Val	Ile	Asp	Cys	115	120	125	
Gly	Asn	Ala	Gly	Ser	Cys	Glu	Gly	Gly	Asn	Asp	Leu	Pro	Val	Trp	Glu	130	135	140	
Tyr	Ala	His	Lys	His	Gly	Ile	Pro	Asp	Glu	Thr	Cys	Asn	Asn	Tyr	Gln	145	150	155	160
Ala	Lys	Asp	Gln	Asp	Cys	Asp	Lys	Phe	Asn	Gln	Cys	Gly	Thr	Cys	Thr	165	170	175	
Glu	Phe	Lys	Glu	Cys	His	Thr	Ile	Gln	Asn	Tyr	Thr	Leu	Trp	Arg	Val	180	185	190	
Gly	Asp	Tyr	Gly	Ser	Leu	Ser	Gly	Arg	Glu	Lys	Met	Met	Ala	Glu	Ile	195	200	205	
Tyr	Ala	Asn	Gly	Pro	Ile	Ser	Cys	Gly	Ile	Met	Ala	Thr	Glu	Met	Met	210	215	220	
Ser	Asn	Tyr	Thr	Gly	Gly	Ile	Tyr	Ala	Glu	His	Gln	Asp	Gln	Ala	Val	225	230	235	240
Ile	Asn	His	Ile	Ile	Ser	Val	Ala	Gly	Trp	Gly	Val	Ser	Asn	Asp	Gly	245	250	255	
Ile	Glu	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp	Gly	Glu	Pro	Trp	Gly	Glu	260	265	270	
Lys	Gly	Trp	Met	Arg	Ile	Val	Thr	Ser	Thr	Tyr	Lys	Gly	Gly	Thr	Gly	275	280	285	
Asp	Ser	Tyr	Asn	Leu	Ala	Ile	Glu	Ser	Ala	Cys	Thr	Phe	Gly	Asp	Pro	290	295	300	



Ile Val  
305

<210> 4  
<211> 1480  
<212> DNA  
<213> Homo sapiens

<400> 4  
ctgggcccag gccgaggccg gggcgggatc cagagcggga gccggcgcgg gatctgggac 60  
tcggagcggg atccggagcg ggacccagga gccggcgcgg ggccatggcg aggcgcgggc 120  
caggggtggcg gccgcttctg ctgctcgtgc tgctggcggg cgcggcgcag ggcggcctct 180  
acttccgccg gggacagacc tgctaccggc ctctgcgggg ggacgggctg gctccgctgg 240  
ggcgcagcac atacccccgg cctcatgagt acctgtcccc agcggatctg cccaagagct 300  
gggactggcg caatgtggat ggtgtcaact atgccagcat caccggaac cagcacatcc 360  
cccaatactg cggctcctgc tgggcccacg ccagcaccag cgctatggcg gatcggatca 420  
acatcaagag gaagggagcg tggccctcca cctcctgtc cgtgcagaac gtcacgcact 480  
gcggtaacgc tggctcctgt gaagggggta atgacctgtc cgtgtgggac tacgcccacc 540  
agcacggcat ccctgacgag acctgcaaca actaccaggc caaggaccag gagtgtgaca 600  
agtttaacca atgtgggaca tgcaatgaat tcaaagagtg ccacgccatc cggaactaca 660  
ccctctggag ggtgggagac tacggctccc tctctgggag ggagaagatg atggcagaaa 720  
tctatgcaaa tgggcccatc agctgtggaa taatggcaac agaaagactg gctaactaca 780  
ccggaggcat ctatgccgaa taccaggaca ccacatatat aaaccatgtc gtttctgtgg 840  
ctgggtgggg catcagtgat gggactgagt actggattgt ccggaattca tggggtgaac 900  
catggggcga gagaggctgg ctgaggatcg tgaccagcac ctataaggat ggggaaggcg 960  
ccagatacaa ccttgccatc gaggagcact gtacatttgg ggaccccatc gtttaaggcc 1020  
atgtcactag aagcgcagtt taagaaaagg catggtgacc catgaccaga ggggatccta 1080  
tggttatgtg tgccaggctg gctggcagga actggggtgg ctatcaatat tggatggcga 1140  
ggacagcgtg gcactggctg cgagtgttcc tgagagttga aagtgggatg acttatgaca 1200  
cttgcacagc atggctctgc ctcaaatga tgcagtcagc cacctgggtga agaagtgacc 1260  
tgcgacacag gaaacgatgg gacctcagtc ttcttcagca gaggacttga tattttgtat 1320  
ttggcaactg tgggcaataa tatggcattt aagaggtgaa agagttcaga cttatcacca 1380  
ttcttatgtc actttagaat caaggggtggg ggagggaggg agggagttgg cagtttcaaa 1440

tcgcccaagt gatgaataaa gtatctggct ctgcacgaga

1480

<210> 5

<211> 303

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Arg Arg Gly Pro Gly Trp Arg Pro Leu Leu Leu Leu Val Leu  
1 5 10 15

Leu Ala Gly Ala Ala Gln Gly Gly Leu Tyr Phe Arg Arg Gly Gln Thr  
20 25 30

Cys Tyr Arg Pro Leu Arg Gly Asp Gly Leu Ala Pro Leu Gly Arg Ser  
35 40 45

Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu Pro Lys  
50 55 60

Ser Trp Asp Trp Arg Asn Val Asp Gly Val Asn Tyr Ala Ser Ile Thr  
65 70 75 80

Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala His Ala  
85 90 95

Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys Gly Ala  
100 105 110

Trp Pro Ser Thr Leu Leu Ser Val Gln Asn Val Ile Asp Cys Gly Asn  
115 120 125

Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Ser Val Trp Asp Tyr Ala  
130 135 140

His Gln His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln Ala Lys  
145 150 155 160

Asp Gln Glu Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Asn Glu Phe  
165 170 175

Lys Glu Cys His Ala Ile Arg Asn Tyr Thr Leu Trp Arg Val Gly Asp  
180 185 190

Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile Tyr Ala  
 195 200 205

Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Arg Leu Ala Asn  
 210 215 220

Tyr Thr Gly Gly Ile Tyr Ala Glu Tyr Gln Asp Thr Thr Tyr Ile Asn  
 225 230 235 240

His Val Val Ser Val Ala Gly Trp Gly Ile Ser Asp Gly Thr Glu Tyr  
 245 250 255

Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu Arg Gly Trp  
 260 265 270

Leu Arg Ile Val Thr Ser Thr Tyr Lys Asp Gly Lys Gly Ala Arg Tyr  
 275 280 285

Asn Leu Ala Ile Glu Glu His Cys Thr Phe Gly Asp Pro Ile Val  
 290 295 300

<210> 6  
 <211> 646  
 <212> DNA  
 <213> Murinae gen. sp.

<400> 6  
 tcctttccta gtctgtcttc agatgaaacc tattctctgc ttgtacaaga accagtagcc 60  
 gtcctcaagg ccaacagcgt tggggagcgt tacgaggttt agagacgttt agccagttag 120  
 tttaaccaaga ctctttcggg actttcacca tcaatgaatc cagtatagct gattctccaa 180  
 gattccctca tagaggaatt ttaattgata catctagaca cttctgcct gtgaagacaa 240  
 ttttaaaaac tctggatgcc atggctttta ataagtttaa tggtcttcac tggcacatag 300  
 tggacgacca gtctttccct tatcagagta ccacttttcc tgagctaagc aataagggaa 360  
 gctactcttt gtctcatgtc tatacaccaa acgatgtccg gatgggtgctg gagtacgccc 420  
 ggctccgagg gattcgagtc ataccagaat ttgatacccc tggccataca cagtcttggg 480  
 gcaaaggaca gaaaaacctt ctaactccat gttacaatca aaaaactaaa actcaagtgt 540  
 ttgggcctgt agaccaact gtaaacacaa cgtatgcatt ctttaacaca tttttcaaag 600

aaatcagcag tgtgtttcca gatcagttca tccacttggg aggaga

646

<210> 7

<211> 1805

<212> DNA

<213> Murinae gen. sp.

<400> 7

ggatgctttc ttcccagcga cccagactgg aagggtgggc caaagactgc ctagccagac 60

tcgcggagca gtcatgccgc agtccccgcg tagcgcccc gggctgctgc tgctgcaggc 120

gctgggtgctg ctagtgctgc tggccctagt gggcccgccc cgactgcaac ctgcgctatg 180

gcccttcccc cgctcggctgc agatgttccc gcggctgttg tacatctccg cggaggactt 240

cagcatcgac cacagtccca attccacagc gggcccttcc tgctcgtgc tacaggaggc 300

gtttcggcga tattacaact atgtttttgg tttctacaag agacatcatg gccctgctag 360

atttcgagct gagccacagt tgcagaagct cctgggtctcc attaccctcg agtcagagtg 420

cgagtccttc cctagtctgt cttcagatga aacctattct ctgcttgtag aagaaccagt 480

agccgtcctc aaggccaaca gcgtttgggg agcgttacga ggtttagaga cgtttagcca 540

gttagtttac caagactctt tcgggacttt caccatcaat gaatccagta tagctgattc 600

tccaagattc cctcatagag gaattttaat tgatacatct agacacttcc tgccctgtgaa 660

gacaatttta aaaactctgg atgccatggc ttttaataag tttaatgttc ttcactggca 720

catagtggac gaccagtctt tcccttatca gagtaccact tttcctgagc taagcaataa 780

gggaagctac tctttgtctc atgtctatac accaaacgat gtccggatgg tgctggagta 840

cgccccggctc cgagggattc gagtcatacc agaatttgat acccctggcc atacacagtc 900

ttggggcaaa ggacagaaaa accttctaac tccatgttac aatcaaaaaa ctaaaactca 960

agtgtttggg cctgtagacc caactgtaaa cacaacgtat gcattcttta acacattttt 1020

caaagaaatc agcagtgtgt ttccagatca gttcatccac ttgggaggag atgaagtaga 1080

atttcaatgt tgggcatcaa atccaaacat ccaaggtttc atgaagagaa agggcttttg 1140

cagcgatttt agaagactag aatcctttta tattaaaaag attttgaaa ttatttcac 1200

cttaaagaag aactccattg tttggcaaga agtttttgat gataaggtag agcttcagcc 1260

gggcacagta gtcgaagtgt ggaagagtga gcattattca tatgagctaa agcaagtcac 1320

aggctctggc ttccctgcc tctttctgc tcttggtac ttagacctga tcagctatgg 1380

gcaagactgg aaaaactact acaaagttga gcccttaat tttgaaggct ctgagaagca 1440

gaaacaactt gttattggtg gagaagcttg cctgtgggga gaatttgtgg atgcaactaa 1500  
 ccttactcca agattatggc ctgagcaag cgctgttggg gagagactct ggagccctaa 1560  
 aactgtcact gacctagaaa atgcctacaa acgactggcc gtgcaccgct gcagaatggt 1620  
 cagccgtgga atagctgcac aacctctcta tactggatac tgtaactatg agaataaaat 1680  
 atagaagtga cagacgtcta cagcattcca gctatgatca tgttgattct gaaatcatgt 1740  
 aaattaagat ttgttaggct gttttttttt taaataaacc atctttttat tgattgaatc 1800  
 tttct 1805

<210> 8  
 <211> 536  
 <212> PRT  
 <213> Murinae gen. sp.

<400> 8

Met Pro Gln Ser Pro Arg Ser Ala Pro Gly Leu Leu Leu Leu Gln Ala  
 1 5 10 15

Leu Val Ser Leu Val Ser Leu Ala Leu Val Ala Pro Ala Arg Leu Gln  
 20 25 30

Pro Ala Leu Trp Pro Phe Pro Arg Ser Val Gln Met Phe Pro Arg Leu  
 35 40 45

Leu Tyr Ile Ser Ala Glu Asp Phe Ser Ile Asp His Ser Pro Asn Ser  
 50 55 60

Thr Ala Gly Pro Ser Cys Ser Leu Leu Gln Glu Ala Phe Arg Arg Tyr  
 65 70 75 80

Tyr Asn Tyr Val Phe Gly Phe Tyr Lys Arg His His Gly Pro Ala Arg  
 85 90 95

Phe Arg Ala Glu Pro Gln Leu Gln Lys Leu Leu Val Ser Ile Thr Leu  
 100 105 110

Glu Ser Glu Cys Glu Ser Phe Pro Ser Leu Ser Ser Asp Glu Thr Tyr  
 115 120 125

Ser Leu Leu Val Gln Glu Pro Val Ala Val Leu Lys Ala Asn Ser Val  
 130 135 140

Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser Gln Leu Val Tyr Gln  
145 150 155 160

Asp Ser Phe Gly Thr Phe Thr Ile Asn Glu Ser Ser Ile Ala Asp Ser  
165 170 175

Pro Arg Phe Pro His Arg Gly Ile Leu Ile Asp Thr Ser Arg His Phe  
180 185 190

Leu Pro Val Lys Thr Ile Leu Lys Thr Leu Asp Ala Met Ala Phe Asn  
195 200 205

Lys Phe Asn Val Leu His Trp His Ile Val Asp Asp Gln Ser Phe Pro  
210 215 220

Tyr Gln Ser Thr Thr Phe Pro Glu Leu Ser Asn Lys Gly Ser Tyr Ser  
225 230 235 240

Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg Met Val Leu Glu Tyr  
245 250 255

Ala Arg Leu Arg Gly Ile Arg Val Ile Pro Glu Phe Asp Thr Pro Gly  
260 265 270

His Thr Gln Ser Trp Gly Lys Gly Gln Lys Asn Leu Leu Thr Pro Cys  
275 280 285

Tyr Asn Gln Lys Thr Lys Thr Gln Val Phe Gly Pro Val Asp Pro Thr  
290 295 300

Val Asn Thr Thr Tyr Ala Phe Phe Asn Thr Phe Phe Lys Glu Ile Ser  
305 310 315 320

Ser Val Phe Pro Asp Gln Phe Ile His Leu Gly Gly Asp Glu Val Glu  
325 330 335

Phe Gln Cys Trp Ala Ser Asn Pro Asn Ile Gln Gly Phe Met Lys Arg  
340 345 350

Lys Gly Phe Gly Ser Asp Phe Arg Arg Leu Glu Ser Phe Tyr Ile Lys  
355 360 365

Lys Ile Leu Glu Ile Ile Ser Ser Leu Lys Lys Asn Ser Ile Val Trp  
370 375 380

Gln Glu Val Phe Asp Asp Lys Val Glu Leu Gln Pro Gly Thr Val Val  
385 390 395 400

Glu Val Trp Lys Ser Glu His Tyr Ser Tyr Glu Leu Lys Gln Val Thr  
405 410 415

Gly Ser Gly Phe Pro Ala Ile Leu Ser Ala Pro Trp Tyr Leu Asp Leu  
420 425 430

Ile Ser Tyr Gly Gln Asp Trp Lys Asn Tyr Tyr Lys Val Glu Pro Leu